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Sequence Listing was accepted with existing errors.

See attached Validation Report.

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Reviewer: MSpencer

Timestamp: Mon May 07 12:02:37 EDT 2007

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Application No: 10573245

Version No: 1.0

Input Set:

Output Set:

Started: 2007-04-20 12:00:24.452  
Finished: 2007-04-20 12:00:24.973  
Elapsed: 0 hr(s) 0 min(s) 0 sec(s) 521 ms  
Total Warnings: 1  
Total Errors: 1  
No. of SeqIDs Defined: 24  
Actual SeqID Count: 24

ErrCode	Error Description
E 320	Wrong Nucleic Acid Designator, gab in SEQID (5)
W 213	Artificial or Unknown found in <213> in SEQ ID (8)

# SEQUENCE LISTING

<110> The University of York

<120> Expansion Polypeptides

<130> 2902076.1

<140> 10573245

<141> 2007-05-07

<150> 10/573,245

<151> 2006-03-23

<150> PCT/GB04/04058

<151> 2004-08-23

<160> 24

<170> PatentIn version 3.4

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<212> DNA

<213> Craterostigma plantagineum

<220>

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Thr Ser Ser Ser His Phe Ala Arg Ala Tyr Tyr Gly Gly Asp Gly Gly

20 25 30

tgg acc gat gcg cat gcg acc ttt tat ggc ggc agc gat gcg agc ggc 144

Trp Thr Asp Ala His Ala Thr Phe Tyr Gly Gly Ser Asp Ala Ser Gly

35 40 45

acc atg ggc ggc gcg tgc ggc tat ggc aac ctg tat agc cag ggc tat 192

Thr Met Gly Gly Ala Cys Gly Tyr Gly Asn Leu Tyr Ser Gln Gly Tyr

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ggc acc aac acc gcg gcg ctg agc acc gcg ctg ttt aac aac ggc ctg 240

Gly Thr Asn Thr Ala Ala Leu Ser Thr Ala Leu Phe Asn Asn Gly Leu

65 70 75 80

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Ser Cys Gly Ser Cys Phe Glu Ile Lys Cys Ala Ser Ser Ile Ser Gly

85 90 95

ggc ggc aaa tgg tgc ctg ccg ggc ggc agc att acc gtg acc gcg acc	336
Gly Gly Lys Trp Cys Leu Pro Gly Gly Ser Ile Thr Val Thr Ala Thr	
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aac ttt tgc ccg ccg aac aac gcg ctg ccg aac aac gcg ggc ggc tgg	384
Asn Phe Cys Pro Pro Asn Asn Ala Leu Pro Asn Asn Ala Gly Gly Trp	
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Cys Asn Pro Pro Leu Gln His Phe Asp Leu Ser Gln Pro Val Phe Gln	
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165170175	
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Ser Tyr Phe Asn Leu Val Leu Ile Thr Asn Val Gly Gly Ala Gly Asp	
180185190	
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Val His Ala Val Ser Ile Lys Gly Ala Thr Thr Asp Trp Gln Pro Met	
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210215220	
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Gln Arg Leu Ser Phe Lys Val Thr Thr Ser Asp Gly Arg Thr Leu Val	
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Thr	Met	Gly	Gly	Ala	Cys	Gly	Tyr	Gly	Asn	Leu	Tyr	Ser	Gln	Gly	Tyr		
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Ser	Cys	Gly	Ser	Cys	Phe	Glu	Ile	Lys	Cys	Ala	Ser	Ser	Ile	Ser	Gly		
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145					150					155					160		
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			180					185						190			
Val	His	Ala	Val	Ser	Ile	Lys	Gly	Ala	Thr	Thr	Asp	Trp	Gln	Pro	Met		
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225					230					235					240		
Ser	Asn	Asn	Val	Ala	Pro	Pro	Asn	Trp	Ser	Phe	Gly	Gln	Thr	Phe	Ala		
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tgc ggc tat ggc aac ctg tat agc acc ggc tat ggc acc aac acc gcg 96  
Cys Gly Tyr Gly Asn Leu Tyr Ser Thr Gly Tyr Gly Thr Asn Thr Ala  
20 25 30  
  
gcg ctg agc acc gcg ctg ttt aac aac ggc ctg acc tgc ggc gcg tgc 144  
Ala Leu Ser Thr Ala Leu Phe Asn Asn Gly Leu Thr Cys Gly Ala Cys  
35 40 45  
  
tat gaa ctg acc tgc aac aac gat ccg cgc ggc tgg tgc ctg agc ggc 192  
Tyr Glu Leu Thr Cys Asn Asn Asp Pro Arg Gly Trp Cys Leu Ser Gly  
50 55 60  
  
acc att atg gtg acc gcg acc aac ttt tgc ccg ccg aac ccg agc ctg 240  
Thr Ile Met Val Thr Ala Thr Asn Phe Cys Pro Pro Asn Pro Ser Leu  
65 70 75 80  
  
ccg aac gat aac ggc ggc tgg tgc aac ccg ccg cgc cag cat ttt gat 288  
Pro Asn Asp Asn Gly Gly Trp Cys Asn Pro Pro Arg Gln His Phe Asp  
85 90 95  
  
ctg gcg gaa ccg gcg ttt ctg cag att gcg cag tat aaa gcg ggc att 336  
Leu Ala Glu Pro Ala Phe Leu Gln Ile Ala Gln Tyr Lys Ala Gly Ile  
100 105 110  
  
gtg ccg gtg aac tat cgc cgc gtg ccg tgc cag aaa aaa ggc ggc att 384  
Val Pro Val Asn Tyr Arg Arg Val Pro Cys Gln Lys Lys Gly Gly Ile  
115 120 125  
  
cgc ttt acc att aac ggc cat agc ttt ttt aac ctg gtg ctg gtg acc 432  
Arg Phe Thr Ile Asn Gly His Ser Phe Phe Asn Leu Val Leu Val Thr  
130 135 140  
  
aac gtg ggc ggc gtg ggc gat gtg cat agc gtg agc att aaa ggc agc 480  
Asn Val Gly Gly Val Gly Asp Val His Ser Val Ser Ile Lys Gly Ser  
145 150 155 160

aac ggc ggc tgg cag ccg ctg agc cgc aac tgg ggc cag aac tgg cag  
Asn Gly Gly Trp Gln Pro Leu Ser Arg Asn Trp Gly Gln Asn Trp Gln  
165170175

agc aac agc tat ctg aac ggc cag agc ctg agc ttt cag gtg acc acc  
Ser Asn Ser Tyr Leu Asn Gly Gln Ser Leu Ser Phe Gln Val Thr Thr  
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agc gat ggc cgc acc gtg acc agc tat gat gtg gcg ccg cgc ggc tgg  
Ser Asp Gly Arg Thr Val Thr Ser Tyr Asp Val Ala Pro Arg Gly Trp  
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354045

Tyr Glu Leu Thr Cys Asn Asn Asp Pro Arg Gly Trp Cys Leu Ser Gly  
505560

Thr Ile Met Val Thr Ala Thr Asn Phe Cys Pro Pro Asn Pro Ser Leu  
65707580

Pro Asn Asp Asn Gly Gly Trp Cys Asn Pro Pro Arg Gln His Phe Asp  
859095

Leu Ala Glu Pro Ala Phe Leu Gln Ile Ala Gln Tyr Lys Ala Gly Ile  
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Val Pro Val Asn Tyr Arg Arg Val Pro Cys Gln Lys Lys Gly Gly Ile  
115120125

Arg Phe Thr Ile Asn Gly His Ser Phe Phe Asn Leu Val Leu Val Thr

130

135

140

Asn Val Gly Gly Val Gly Asp Val His Ser Val Ser Ile Lys Gly Ser  
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Asn Gly Gly Trp Gln Pro Leu Ser Arg Asn Trp Gly Gln Asn Trp Gln  
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Ser Asn Ser Tyr Leu Asn Gly Gln Ser Leu Ser Phe Gln Val Thr Thr  
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Gly Ala Cys Gly Tyr Gly Asn Leu Tyr Ser Gln Gly Tyr Gly Thr Asn  
202530

96

acc gcg gcg ctg agc acc acc ctg ttt aac aac ggc ctg gcg tgc ggc  
Thr Ala Ala Leu Ser Thr Thr Leu Phe Asn Asn Gly Leu Ala Cys Gly  
354045

144

agc tgc tat cag gtg cgc tgc gaa ggc ggc ccg aaa tgg tgc gtg cgc  
Ser Cys Tyr Gln Val Arg Cys Glu Gly Gly Pro Lys Trp Cys Val Arg  
505560

192

ggc ggc gat cgc att att acc gtg acc gcg acc aac ttt tgc ccg ccg  
Gly Gly Asp Arg Ile Ile Thr Val Thr Ala Thr Asn Phe Cys Pro Pro  
65707580

240

aac tat gcg ctg gcg aac gat aac ggc ggc tgg tgc aac ccg ccg cgc  
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859095

288



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Gln His Phe Asp Met Ala Gln Pro Ala Phe Val Arg Ile Ala His Tyr	
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cgc gcg ggc att gtg ccg att agc tat cgc cgc gtg agc tgc gtg aaa	384
Arg Ala Gly Ile Val Pro Ile Ser Tyr Arg Arg Val Ser Cys Val Lys	
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aaa ggc ggc att cgc ctg acc att aac ggc cat agc tat ttt aac ctg	432
Lys Gly Gly Ile Arg Leu Thr Ile Asn Gly His Ser Tyr Phe Asn Leu	
130135140	
gtg ctg gtg agc aac gtg ggc ggc agc ggc gat gtg cat gcg gtg tgg	480
Val Leu Val Ser Asn Val Gly Gly Ser Gly Asp Val His Ala Val Trp	
145150155160	
att aaa ggc agc ggc ggc ggc ccg tgg cag gcg atg acc cgc aac tgg	528
Ile Lys Gly Ser Gly Gly Gly Pro Trp Gln Ala Met Thr Arg Asn Trp	
165170175	
ggc cag aac tgg cag agc aac agc tat ctg gat ggc cag agc ctg agc	576
Gly Gln Asn Trp Gln Ser Asn Ser Tyr Leu Asp Gly Gln Ser Leu Ser	
180185190	
ttt att gtg cgc gcg ggc gat ggc cgc acc gtg acc gcg aac gab att	624
Phe Ile Val Arg Ala Gly Asp Gly Arg Thr Val Thr Ala Asn Xaa Ile	
195200205	
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202530	
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354045	

Ser Cys Tyr Gln Val Arg Cys Glu Gly Gly Pro Lys Trp Cys Val Arg  
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Gly Gly Asp Arg Ile Ile Thr Val Thr Ala Thr Asn Phe Cys Pro Pro  
65 70 75 80

Asn Tyr Ala Leu Ala Asn Asp Asn Gly Gly Trp Cys Asn Pro Pro Arg  
85 90 95

Gln His Phe Asp Met Ala Gln Pro Ala Phe Val Arg Ile Ala His Tyr  
100 105 110

Arg Ala Gly Ile Val Pro Ile Ser Tyr Arg Arg Val Ser Cys Val Lys  
115 120 125

Lys Gly Gly Ile Arg Leu Thr Ile Asn Gly His Ser Tyr Phe Asn Leu  
130 135 140

Val Leu Val Ser Asn Val Gly Gly Ser Gly Asp Val His Ala Val Trp  
145 150 155 160

Ile Lys Gly Ser Gly Gly Gly Pro Trp Gln Ala Met Thr Arg Asn Trp  
165 170 175

Gly Gln Asn Trp Gln Ser Asn Ser Tyr Leu Asp Gly Gln Ser Leu Ser  
180 185 190

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195 200 205

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